REMARKS

1. Introduction

1.1. The claims, both examined and withdrawn, have been amended so that the microorganism is limited to S. cerevisiae.

1.2. We believe that microorganism claim 1 is allowable and that the restricted-out method claims, now being directly or indirectly dependent thereon, should be rejoined pursuant to MPEP 821.04.

2. 35 USC 112 Requirements Generally

2.1. The Examiner's "written description" and "enablement" rejection assume that the claims as examined cover mutants of PGM2 as well as wild-type PGM2. We know of no reasonable basis for this assumption and we hereby state for the record that the term "PGM2" as used in claim 1 means exactly that, the wild-type enzyme.

Indeed, in the last amendment, page 8, we stated, "by the present amendment, the enzyme is restricted now to PGM2, an enzyme of completely known structure".

Claim 1 recites "over expressing PGM2", not "wild-type PGM2 or a mutant thereof". The increased level of galactose uptake rate is attributable to the overexpression, and the overexpression is the result of changes in the control sequence, and/or in the copy number. The wild-type PGM2 protein can be expressed (over overexpressed) by recombinant DNA methods, with changes in the promoter or the gene copy number as contemplated by claim 1. Mutation is not necessary to change the level of galactose uptake rate.

Reviewing the specification, we of course have teachings that one may use of mutated form of an enzyme (P6, L3), which was the basis for claim 7. The parental enzyme could be PGM2.

However, nowhere is "PGM2" expressly defined as including mutants of wild-type PGM2. Hence, it seems to Applicant that "PGM2" as it appears in claim 1 must be interpreted as referring

to the wild-type enzyme.

The written description and enablement rejections concede that applicants have an adequate written description, and an enabling disclosure, for wild type PGM2 in S. cerevisiae.

Since for the reasons set forth above, the term "PGM2" in claim 1 is properly construed as limited to what the Examiner calls "wild type PGM2", and claim 1 has now been amended (under protest), to require S. cerevisiae as the microorganism, it follows that claim 1 fully satisfies the written description and enablement requirements, and that it, and all dependent claims (4-6, 9-12, 15, 17, 21-25) should now be allowed.

2.2. Applicants have added a new claim 26 which is like amended claim 1 except that after "PGM2", it recites ", or a mutant thereof...." The presentation of this new claim does not raise new issues requiring further consideration and search because the Examiner already examined (albeit unnecessarily) the issues of written description and enablement for mutants of PGM2.

Note that the Examiner's rejections are now relevant only to this new claim 26.

The basis for the presentation of this new claim 26 is in the combination of original claims 3 (reciting PGM2) and 7 (reciting a gene coding for a mutated form of an enzyme), as well as page 6, lines 2-6.

While the term "PGM2 mutant" is not explicitly defined in terms of a particular percentage sequence identity to the PGM2 amino acid sequence, it must be noted that the specification recognizes PGM1 and PGM2 as distinct entities, see, e.g., page 5, lines 26-27; page 3, lines 7 and 16-17. Hence, it follows that the term "PGM2 mutant" cannot be construed so broadly as to encompass PGM2 (let alone more distant enzymes such as AGM or PMM, cited at page 14 of the May 22, 2006 office action[1]).

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[1] If the term "PGM mutant" were so broadly construed, then the claim would have to be considered supported by four enzymes (PGM1, PGM2, AGM and PMM), whose complete structures were known, which would in turn affect the analysis of the generic claim.

Enclosed (Ex. A) is the result of a BlastP search using S. cerevisiae PGM2 (P37012) as the query sequence. There is 78% identity and 89% similarity with S. cerevisiae PGM1 (P33401).

Presumably, for a mutant to be considered a "PGM2 mutant" (rather than a "PGM1 mutant") it would need to have a higher degree of identity with wild-type PGM2 than with wild-type PGM1. That implies an identity exceeding 89% (100-(100-78)/2).

2.3. The Examiner's "response to arguments" doesn't clearly differentiate the written description and enablement rejections, even though they apply different legal standards. For example, the "possession" standard mentioned at the bottom of page 8 is applied only in a written description rejection.

While the ultimate standard of written description is "possession", that doesn't mean operability is irrelevant.

In the traditional formulation of written description, the original claims necessarily satisfied the written description requirement. Applicants clearly stated in original claim 1 "being a yeast or other fungi" and therefore clearly had conceived applicability of their invention to fungi other than S. cerevisiae (and likewise to). Likewise, original claim 1 recited an enzyme of particular catalytic activity and original dependent claims 3 and 7 made it clear that the enzyme could be PGM2 and that the enzyme could be a mutant enzyme.

Eli Lilly and related cases placed a quasi-operability gloss on the traditional written description requirement, arguing that written description required disclosure of (1) a complete structure (with exceptions) of a claimed species, and (2) that a genus claim be so supported by a "representative number" of species. **The determination of what is a "representative number" is clearly closely wedded to operability concepts.** For example, is there a known or disclosed correlation between structure and function.

Operability may also be relevant to enablement. The enablement requirement relates to whether there is a disclosure, adequate to one skilled in the art, as to how to make and use the

invention. It has two components. First, the invention must be operable, because if it is inoperable, it is not possible to teach how to use it. Secondly, the invention must be reproducible, without undue experimentation, from the disclosure. Since the standard of undue experimentation is based on the skilled worker, the disclosure is interpreted in the light of the general knowledge of the art.

Formally speaking, if the Examiner questions operability (utility), the Examiner is supposed to make a dual rejection under 35 USC 101 and 112 ¶1. And if an Examiner questions reproducibility (the quality of the disclosure of an operable invention) then the Examiner makes a pure 112 ¶1 rejection. Conceivably, the Examiner could make both a dual 101/112 ¶1 rejection and a pure 112 ¶1 rejection of the same claim. See MPEP 2164.07, and In re Hitchings, 144 USPQ 637, 642 (CCPA 1965). However, it is not exactly unusual for an Examiner to make a 112 rejection which raises operability issues.

The instant enablement rejection admittedly appears directed to reproducibility. That is, the Examiner has not asserted that no mutants of PGM2 exist which would result in a higher specific galactose uptake rate, let alone mutants which achieve a rate which is merely comparable to wild type. Rather, the Examiner's concerns are with reproducibility, that is, would the skilled worker be able, without undue experimentation, to identify functional mutants of PGM2. This issue is analyzed in section 4, below. However, it should be noted that a claimed invention may be reproducible, without undue experimentation, even when an explicit disclosure is absent. For example, the procedure might be a conventional one. Hence, operability can be relevant even to this issue. Conventional procedures may be characterized by a high level of operability.

3. Written Description (OA pp. 4-8)

The claims stand rejected under 35 USC 112 first paragraph for failing to comply with the written description requirement

because, whilst there is admitted to be an adequate written description for wild type PGM2 in *S. cerevisiae*, the description allegedly does not show possession of any recombinant, prototrophic fungus comprising any PGM2 enzyme. As previously noted, this rejection is properly applied (if at all) only to new claim 26.

There are two aspects to the alleged lack of description, centering respectively on the claim coverage extending beyond *S. cerevisiae* and on the claim coverage extending beyond the wild type PGM2 enzyme to 'any PGM2 enzyme'.

Whilst firmly disagreeing with the micro-organism aspect of the rejection, the Applicant has amended the claims to require *S. cerevisiae* as the micro-organism, thus rendering that aspect of the rejection moot.

In a separate "Petition to Withdraw Finality", we have explained why the written description rejection, as applied to claims covering PGM2 mutants, is a new ground of rejection, and hence the instant office action should not have been made final.

Going to the substance of the rejection, it is in our submission improper for the following reasons.

First, it was set out in the office action of 22nd May 2006 on page 8 that to provide adequate description and evidence of possession of a claimed genus, the specification must provide sufficient distinguishing identifying characteristics of the genus, taking into account matters including 'disclosure of a complete or partial structure, physical and/or chemical properties, functional characteristics, structure/function correlation, and any combination thereof'.

The Examiner has not explicitly applied an analysis of these factors to the instant claims.

Clearly, in relation to a mutant PGM2, the description provides a 'partial structure' in that to be a mutant PGM2 implies a close structural relationship with wild type PGM2. Some entirely different enzyme having the required catalytic activity would not be covered. A protein so different in

sequence that those skilled in the art would consider it to be an entirely different enzyme would not be included.

As to physical and/or chemical properties, there is complete description in that the enzyme is necessarily a protein, has defined catalytic ability and physical characteristics that will be similar to those of wild type PGM2. All that is implicit simply in the term 'mutant'.

The functional characteristics of the mutant are described, i.e. the ability to catalyse the recited reaction with a higher than normal specific activity.

The specification states on page 6 that techniques for providing mutants with increased activity (as well as other beneficial techniques for increasing expressed activity) are known in the art, and the Examiner has not challenged the truth of that.

The justification offered by the Examiner in the current office action is in part copied and pasted from an earlier action in which it was written in respect of a different claim. Thus, it is not apparent how it is relevant to the present claims that the art recognizes four enzymes having the specified catalytic action. None of PGM1, AGM or PMM are mutant forms of PGM2. Of course it may be fairly be pointed out that even though these proteins are not considered "mutants of PGM2", and thus must be more divergent in structure from wild type PGM2 then any "PGM2 mutant", they nonetheless provide the specified catalytic activity.

The Examiner has alleged that it would be '*unknown to one skilled in the art which functions of PGM2 are required such that galactose uptake rate is increased*'. However, the Examiner has not demonstrated that PGM2 has different functions from which a choice can be made. It is described in the specification only as catalysing the conversion of glucose-1 phosphate to glucose-6 phosphate. Accordingly, the skilled reader would understand from the description that it is this catalytic function that needs to be increased if a mutant is to achieve the desired effect, which

is exactly what page 6 in any case states.

However, the issue in respect of the present claims is not merely whether there is sufficient description of a mutant having increased activity, because no such mutant is recited in the claims. The issue includes the question of whether a claim directed to a genus requires description of all members of the genus or is sufficiently described if some members are described.

The Examiner's original rejection of claim 7 was based on the contention that whilst the genus of mutant enzymes of increased activity was 'named', no member of it was described.

In relation to claim 1, that is clearly not the case. The claim embraces both the use of the wild type enzyme and that of functional mutants. Thus, the Examiner must consider whether the wild type PGM2 is "representative" of the claimed genus, which in turn depends on the ease with which mutants which retain the stated activity may be obtained. It should be noted that while the principal commercial reason for using a mutant enzyme would be because it had a higher specific activity, the claim does not in fact require higher activity; it can be the same as wild-type or even less (provided that in conjunction with the choice of promoter and copy number, there is still increased level of galactose uptake rate). It has not been urged that there would be difficulty in making many mutant enzymes which are functional to no greater extent than the wild type enzyme.

There is no basis in the wording of the section or in the case law for seizing upon some portion of the claim selected by the Examiner, but not identified by the claim as such, and objecting that such a portion of the claim is not particularly described.

On the contrary, the written description guidelines state that there is a strong presumption that original claim language (see original claim 3, "PGM2") is "possessed". Moreover, the guidelines state in footnote 51 that in the genetic arts, it is not necessary that the amino acid sequences of all claimed proteins be determinable from the specification alone.

Training Materials Example 14 is further instructive. It is directed to a protein of defined activity which is of a defined sequence (equivalent here to wild type PGM2) or a variant thereof having at least 95% identity to the wild-type sequence, and the required enzymatic activity. The PTO opined that the inclusion of variants didn't amount to a genus characterized by substantial variation, and the reference sequence was representative of these genus, because of the activity and 95% identity limitations.

However, the PTO did not state that 95% identity was a minimum requirement. Indeed, the PTO has issued claims in which the minimum identity was much lower (e.g., 40% in USP 5,304,640 claim 2 and Bell, USP 4,761,371 claim 8; 50% in Colman USP 5,663,294 claim 1; 55% in Tripp, USP 5,681,724 claim 1) and indeed outside the range at which the protein would be considered a "mutant" of the wild type.

The specification here recognizes PGM1 and PGM2 as different proteins (more precisely, different isoforms of Gal5), see page 3, line 7; page 5, lines 26-27; page 13, line 6) and hence "PGM2 mutants" cannot read upon PGM1. Likewise PGM2 is distinguishable from GAL1, GAL2, GAL7 and GAL10 (P3, L8).

Generally, it will always be possible to identify an area within a claim, which is not specifically picked out in the claim, which the specification does not describe in particular terms. A mechanical device containing a spring may be described and claimed for its improved design and function. The spring may be exemplified as being of steel. The possibility exists that it may be possible to develop steels or other metals for making springs that are superior, but it would be unreasonable to demand limitation of the claims to exclude such yet to be developed materials in the claimed device.

In general, however well an invention is described in any field, there will be a myriad of embodiments of the invention that are not specifically described.

The Guidelines in respect of written description state that

for a claim drawn to a genus, one must look to see whether there is sufficient description of a representative number of species by for instance disclosure of relevant identifying characteristics. Here, the description clearly provides PGM2 in its wild type form and also the concept of mutations. The claim contains activity limitation, so the only mutants embraced by the claims are those which are functional. Accordingly, a representative number of species of the whole scope of the claim is provided. The common attributes and features in question here are a structural relationship with PGM2, such that the variants are still reasonably termed PGM2, and the required enzyme activity.

The message to take from these materials is that one should look to see not whether some particular corner of the claim selected by the Examiner is described but whether in general the subject matter of the claim is representatively described. It is a matter of proportionality. In this case, the claim is not concerned particularly with mutants in the sense that the invention depends on or favors them. The core subject matter is the use of wild type PGM2. That is fully sufficient for working the invention. Still less is the invention especially concerned with mutants having greater than wild type enzymatic activity. Most mutants of working enzymes will be functionally identical to the original enzyme. The skilled artisan will be able to make many conservative changes to a starting enzyme without materially affecting its function for the better or for the worse. The class of mutants identified by the Examiner as lacking description form only a trivial and inessential part of the claim scope and the rejection of the claim is out of line with established practice, irrespective of whether the skilled artisan is able to envisage of what such enzymes would consist.

Secondly, it is of course not the case that the skilled artisan actually needs instruction from the Applicant as to how to prepare mutant enzymes having increased activity. Methods for this are well known. These methods of course include directed

evolution methods that basically operate by introducing random changes in the gene for the enzyme by methods such as error prone PCR, DNA shuffling, or a staggered extension process, cloning into a suitable vector, and selecting for expression of an improved enzyme. The selection in this case would be for higher conversion efficiency and could be conducted by high throughput screening. Alternatively, evolutionary pressure can be applied by expressing the gene in an organism under culture conditions where survival is improved by the ability to carry out the relevant enzyme catalysed conversion. An improved enzyme can then be used as the starting point in a further round of evolution.

This was a very well known technique prior to the filing date. There are about 220 hits on PubMed for pre-filing date papers featuring the key words 'enzyme' and 'directed evolution'. The specification contains instruction that known methodologies for increasing the expression of the relevant enzyme activity (including by selecting a mutated enzyme of higher activity) should be used.

The skilled artisan did not need further instruction from the Applicant on this.

The Examiner has in part sought to justify the rejection by stating that '*because neither the prior art nor the specification teach which domains/sequences of PGM2 beside those of wild-type PGM2 are required to construct a micro-organism with an increased galactose uptake rate, Applicant has still not described the claimed invention in such a way as to convey … possession of … mutated forms of PGM2 with higher specific activity...*'.

As seen above, knowledge of the critical domains/sequences governing activity is not needed for directed evolution of enzymes to develop enhanced activity by well established methods. However, it is not true that the art lacked knowledge of the location of the active sites in PGM2. Five pre-filing date publications discuss the location in PGM2 and related enzymes of three active sites, namely the 'Active site', the 'Metal ion

binding site' and the 'Sugar binding site'.

The relevant publications are:
Manjunath et al; Plant Physiology, 1998
Whitehouse et al; Mol. Biol. Evol. 1998
Levin et al; Protein Engineering, 1999
Videira et al; Applied and Environmental Microbiology; May 2000
Periappuram et al; Plant Physiology, April 2000

Figure 2 of Videira et al contains a particularly clear illustration of this.

The Examiner also comments that '*Neither the specification nor the prior art form a nexus between PGM2 and GAL2 function such that one of ordinary skill in the art would know which functions of PGM2 are required such that galactose uptake rate is increased.*

The specification makes it very clear that the surprising finding of the invention is that more PGM2 enzyme activity produces a higher galactose uptake rate and that one way of achieving this would be to include a PGM2 mutant that has a higher specific enzyme activity (although this is not needed as the claims further require now in any case that the expression level of the enzyme must be increased).

The concept of a nexus between PGM2 and GAL2 function is purely of the Examiner's invention. The Examiner is indulging in pure speculation here. No functions of PGM2 (aka GAL5) have been identified in the art or the specification, or by the Examiner, other than the catalytic interconversion of glucose-1 phosphate and glucose-6 phosphate.

However, it is unclear how this speculation is germane to the issue of whether the specification needs to contain any written description of mutants having a higher specific enzyme activity or needs to contain more such description than it already does.

4. Enablement (OA pp. 5-8)

The claims stand rejected under 35 USC 112 first paragraph for failing to comply with the enablement requirement because, whilst the claims are admittedly enabling for wild type PGM2 in *S. cerevisiae*, the description allegedly does not enable any recombinant, prototrophic fungus comprising any PGM2 enzyme. Again, we remind the Examiner that this rejection is properly applied, if at all, only to claim 26.

There are two aspects to the alleged lack of enablement, centering respectively on the claim coverage extending beyond *S. cerevisiae* and on the claim coverage extending beyond the wild type PGM2 enzyme to 'any PGM2 enzyme'.

Whilst firmly disagreeing with the microorganism aspect of the rejection, the Applicant has amended the claims to require *S. cerevisiae* as the micro-organism, thus rendering the rejection moot.

The rejection as specified by the Examiner in argument is that the specification is not enabling of a mutant PGM2 enzyme having a higher specific activity than wild type.

The test of lack of enablement is whether the invention as claimed can be worked, without undue experimentation, on the basis of the description. As explained in part previously, the skilled worker is familiar with (1) the complete sequence of PGM2, (2) the three likely active sites of PGM2, (3) the general concept in the art as to what substitutions are likely to be conservative, (4) the general concept in the art that mutations outside the active site are less likely to affect activity, (5) knowledge of the specific differences between PGM2 and the three other proteins having the activity of interest, which could individually be introduced into PGM2, (6) knowledge of methods (such as alanine scanning mutagenesis) of identifying sites tolerant of mutation, and (7) knowledge of "directed evolution" methods of rapidly and simultaneously screening large numbers of mutants.

The use of improved forms of PGM2 is not forbidden but is

not called for by the claims. It represents only a very small part of the scope of the claim. It is not in issue seemingly that the central part (PGM2 per se) of the scope of the claim is enabled. The Examiner is not entitled to narrow the enquiry to one corner of the claim which is not picked out by the claim language. Seldom is any invention claimed at any useful breadth ever described in such detail that every possible material for putting it into effect is taught to the skilled person. To hold the contrary would forbid the validity of any claim within the scope of which it is possible for future workers to make their own dependent inventions.

If one took essentially any case directed to an immunoassay using an antibody of a given specificity, and exemplified by the best antibody in the possession of the applicant, one would be able to argue that the claim was lacking enablement for antibodies of still higher affinity or specificity.

If one had a claim to a method of expressing a previously unknown protein by expressing the relevant gene in a convenient organism such as E. coli, one could then argue that the claim was invalid for lack of enablement of unknown promoter sequences that would provide higher expression. There would essentially be no claim safe from this type of rejection.

Clearly if the Applicant were to be limited to claiming the use of the wild type gene then the resulting patent protection would be of little commercial worth. It would certainly be possible for many separate changes to be made to the amino acid structure of the enzyme without preventing the invention from working.

Neither would the situation have been eased by some more examples. The Examiner would still have been able to assert that the skilled reader would not know how to obtain still better or different enzymes going beyond however many variants had been shown.

Secondly, for the reasons given previously, the skilled person does not need instruction on how to provide improved enzymes using techniques that either do not need information regarding the enzyme's structure or by using the published information describing that structure. The provision of additional enzymes, and even improved enzymes, is enabled.

Respectfully submitted,

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Ex.A

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BLAST 2 software.

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NCBI BLAST program reference [PMID:9254694]:
Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W.,
Lipman D.J.  Gapped BLAST and PSI-BLAST: a new generation of protein
database search programs.  Nucleic Acids Res. 25:3389-3402(1997).

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Query:  569 AA
Date run: 2007-06-21 21:10:40 UTC+0100 on blast01.vital-it.ch
Program: NCBI BLASTP 2.2.16 [Mar-25-2007]
Database: UniProtKB
          4,739,517 sequences; 1,558,448,118 total letters
UniProt Knowledgebase Release 11.1 consists of:
 UniProtKB/Swiss-Prot Release 53.1 of 12-Jun-2007:  270778 entries
 UniProtKB/TrEMBL Release 36.1 of 12-Jun-2007: 4448557 entries
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Taxonomic view | NiceBlast view | Printable view

List of potentially matching sequences

Send selected sequences to Clustal W (multiple alignment) Submit Query Select up to...

☐ Include query sequence

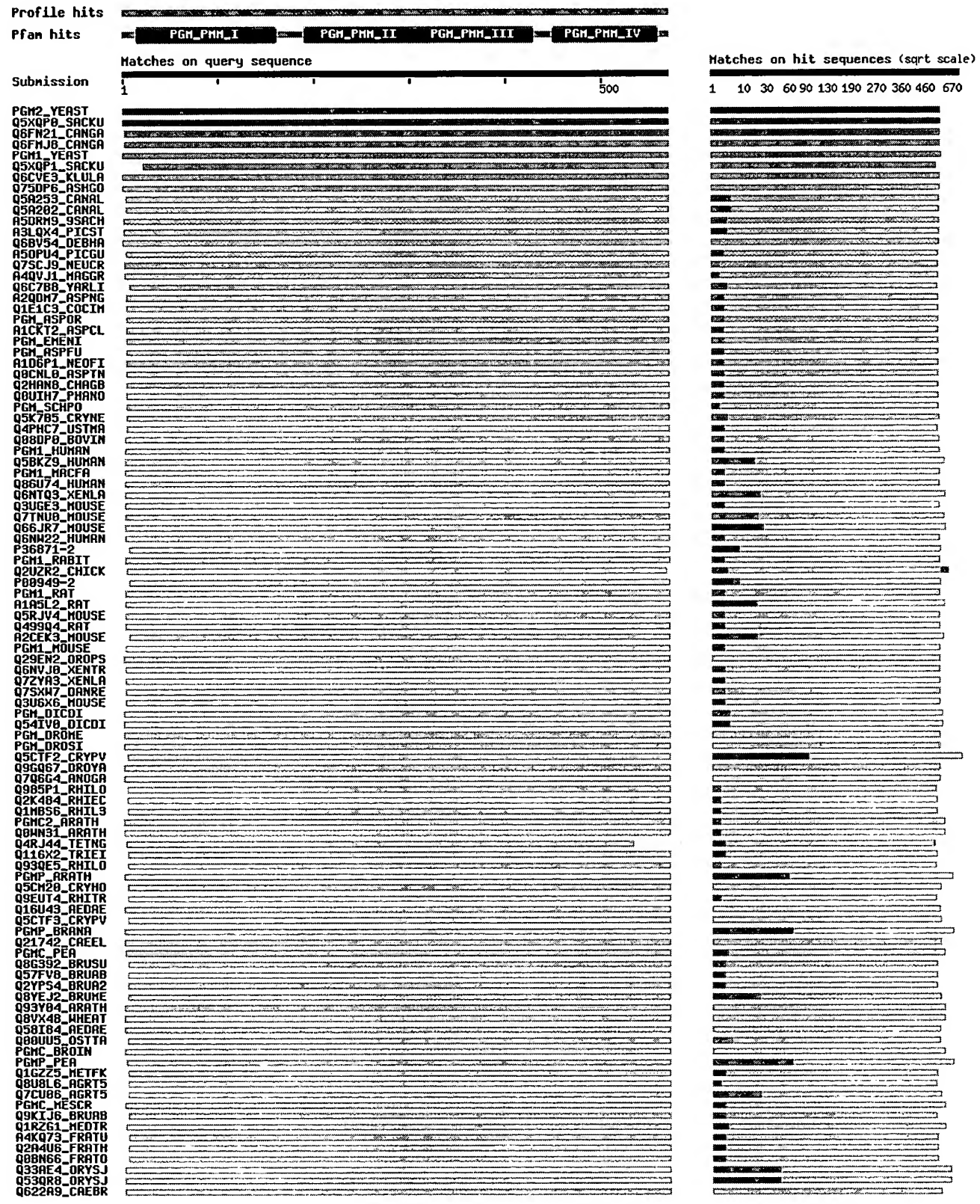
	Db	AC	Description	Score	E-value
☐	sp	P37012	PGM2_YEAST Phosphoglucomutase-2 (EC 5.4.2.2) (Glucose ...	1162	0.0
☐	tr	Q5XQP0	_SACKU PGM2 [Saccharomyces kudriavzevii IFO 1802]	1130	0.0
☐	tr	Q6FN21	_CANGA Similar to sp|P37012 Saccharomyces cerevisiae YM...	977	0.0
☐	tr	Q6FMJ8	_CANGA Similar to sp|P37012 Saccharomyces cerevisiae YM...	977	0.0
☐	sp	P33401	PGM1_YEAST Phosphoglucomutase-1 (EC 5.4.2.2) (Glucose ...	943	0.0
☐	tr	Q5XQP1	_SACKU PGM1 (Fragment) [Saccharomyces kudriavzevii IFO ...	923	0.0
☐	tr	Q6CVE3	_KLULA Similar to sp|P37012 Saccharomyces cerevisiae YM...	871	0.0
☐	tr	Q75DP6	_ASHGO ABL029Wp [ABL029W] [Ashbya gossypii (Yeast) (Ere...	850	0.0
☐	tr	Q5A253	_CANAL Hypothetical protein PGM2 [PGM2] [Candida albica...	758	0.0
☐	tr	Q5A202	_CANAL Hypothetical protein PGM2 [PGM2] [Candida albica...	755	0.0
☐	tr	A5DRM9	_9SACH Phosphoglucomutase [LELG_00015] [Lodderomyces el...	748	0.0
☐	tr	A3LQX4	_PICST Phosphoglucomutase (EC 5.4.2.2) [PGM2] [Pichia s...	731	0.0
☐	tr	Q6BV54	_DEBHA Debaryomyces hansenii chromosome C of strain CBS...	728	0.0
☐	tr	A5DPU4	_PICGU Hypothetical protein [PGUG_05295] [Pichia guilli...	722	0.0
☐	tr	Q7SCJ9	_NEUCR Hypothetical protein NCU10058.1 [NCU10058.1] [Ne...	706	0.0
☐	tr	A4QVJ1	_MAGGR Hypothetical protein [MGG_04495] [Magnaporthe gr...	704	0.0
☐	tr	Q6C7B8	_YARLI Similar to sp|P37012 Saccharomyces cerevisiae YM...	701	0.0
☐	tr	A2QDM7	_ASPNG Catalytic activity: alpha-D-Glucose 1-phosphate ...	701	0.0
☐	tr	Q1E1C3	_COCIM Hypothetical protein [CIMG_03640] [Coccidioides ...	700	0.0
☐	sp	P57749	PGM_ASPOR Phosphoglucomutase (EC 5.4.2.2) (Glucose pho...	697	0.0
☐	tr	A1CKT2	_ASPCL Phosphoglucomutase PgmA [ACLA_039720] [Aspergill...	696	0.0
☐	sp	Q9P931	PGM_EMENI Phosphoglucomutase (EC 5.4.2.2) (Glucose pho...	695	0.0
☐	sp	Q4WY53	PGM_ASPFU Phosphoglucomutase (EC 5.4.2.2) (Glucose pho...	693	0.0
☐	tr	A1D6P1	_NEOFI Phosphoglucomutase PgmA [NFIA_065490] [Neosartor...	691	0.0
☐	tr	Q0CNL0	_ASPTN Phosphoglucomutase [ATEG_04724] [Aspergillus ter...	684	0.0
☐	tr	Q2HAN8	_CHAGB Hypothetical protein [CHGG_02716] [Chaetomium gl...	681	0.0
☐	tr	Q0UIH7	_PHANO Hypothetical protein [SNOG_08437] [Phaeosphaeria...	663	0.0
☐	sp	O74374	PGM_SCHPO Probable phosphoglucomutase (EC 5.4.2.2) (Gl...	656	0.0
☐	tr	Q5K7B5	_CRYNE Phosphoglucomutase, putative (Hypothetical prote...	632	e-179
☐	tr	Q4PHC7	_USTMA Hypothetical protein [UM00486.1] [Ustilago maydi...	625	e-177
☐	tr	Q08DP0	_BOVIN Similar to phosphoglucomutase 1 [MGC143368] [Bos...	551	e-155

☐	sp	P36871	PGM1_HUMAN Phosphoglucomutase-1 (EC 5.4.2.2) (Glucose ...	547 e-154
☐	tr	Q5BKZ9	_HUMAN PGM1 protein (Fragment) [PGM1] [Homo sapiens (Hu...	547 e-154
☐	sp	Q4R5E4	PGM1_MACFA Phosphoglucomutase-1 (EC 5.4.2.2) (Glucose ...	546 e-154
☐	tr	Q86U74	_HUMAN Phosphoglucomutase 1 [Homo sapiens (Human)]	546 e-153
☐	tr	Q6NTQ3	_XENLA LOC414455 protein (Fragment) [LOC414455] [Xenopu...	545 e-153
☐	tr	Q3UGE3	_MOUSE Melanocyte cDNA, RIKEN full-length enriched libr...	543 e-153
☐	tr	Q7TNU0	_MOUSE Pgm2 protein (Fragment) [Pgm2] [Mus musculus (Mo...	543 e-153
☐	tr	Q66JR7	_MOUSE Pgm2 protein (Fragment) [Pgm2] [Mus musculus (Mo...	543 e-153
☐	tr	Q6NW22	_HUMAN Phosphoglucomutase 1 [PGM1] [Homo sapiens (Human)]	543 e-153
☐	sp_vs	P36871-2	Isoform 2 of P36871 - Homo sapiens (Human) [PGM1]...	543 e-152
☐	sp	P00949	PGM1_RABIT Phosphoglucomutase-1 (EC 5.4.2.2) (Glucose ...	543 e-152
☐	tr	Q2UZR2	_CHICK Phosphoglucomutase 1 [Gallus gallus (Chicken)]	542 e-152
☐	sp_vs	P00949-2	Isoform 2 of P00949 - Oryctolagus cuniculus (Rabb...	542 e-152
☐	sp	P38652	PGM1_RAT Phosphoglucomutase-1 (EC 5.4.2.2) (Glucose ph...	541 e-152
☐	tr	A1A5L2	_RAT Pgm1 protein (Fragment) [Pgm1] [Rattus norvegicus ...	541 e-152
☐	tr	Q5RJV4	_MOUSE Phosphoglucomutase 2 [Pgm2] [Mus musculus (Mouse)]	541 e-152
☐	tr	Q499Q4	_RAT Phosphoglucomutase 1 [Pgm1] [Rattus norvegicus (Rat)]	541 e-152
☐	tr	A2CEK3	_MOUSE Phosphoglucomutase 2 [Pgm2] [Mus musculus (Mouse)]	541 e-152
☐	sp	Q9D0F9	PGM1_MOUSE Phosphoglucomutase-1 (EC 5.4.2.2) (Glucose ...	540 e-152
☐	tr	Q29EN2	_DROPS GA18703-PA (Fragment) [Dpse\GA18703] [Drosophila...	539 e-151
☐	tr	Q6NVJ0	_XENTR Phosphoglucomutase 1 [pgm1] [Xenopus tropicalis ...	538 e-151
☐	tr	Q7ZYA3	_XENLA Pgm2-prov protein [Xenopus laevis (African clawe...	538 e-151
☐	tr	Q7SXW7	_DANRE Phosphoglucomutase 1 [pgm1] [Danio rerio (Zebraf...	537 e-151
☐	tr	Q3U6X6	_MOUSE Bone marrow macrophage cDNA, RIKEN full-length e...	536 e-150
☐	sp	Q23919	PGM_DICDI Phosphoglucomutase (EC 5.4.2.2) (Glucose pho...	536 e-150
☐	tr	Q54IV0	_DICDI Phosphoglucomutase A [pgmA] [Dictyostelium disco...	536 e-150
☐	sp	Q9VUY9	PGM_DROME Phosphoglucomutase (EC 5.4.2.2) (Glucose pho...	532 e-149
☐	sp	Q7KHA1	PGM_DROSI Phosphoglucomutase (EC 5.4.2.2) (Glucose pho...	531 e-149
☐	tr	Q5CTF2	_CRYPV Phosphoglucomutase, tandemly duplicated gene (EC...	528 e-148
☐	tr	Q9GQ67	_DROYA Phosphoglucomutase [Pgm] [Drosophila yakuba (Fru...	528 e-148
☐	tr	Q7Q6G4	_ANOGA ENSANGP00000017432 [AgaP_ENSANGG00000014943] [An...	526 e-148
☐	tr	Q985P1	_RHILO Phosphoglucomutase [mlr7590] [Rhizobium loti (Me...	524 e-147
☐	tr	Q2K484	_RHIEC Phosphoglucomutase protein (EC 5.4.2.2) [pgm] [R...	521 e-146
☐	tr	Q1MBS6	_RHIL3 Putative phosphoglucomutase (EC 5.4.2.2) [pgm] [...	520 e-146
☐	sp	Q9SGC1	PGMC2_ARATH Probable phosphoglucomutase, cytoplasmic 2...	520 e-145
☐	tr	Q0WN31	_ARATH Putative phosphoglucomutase [At1g70730] [Arabido...	520 e-145
☐	tr	Q4RJ44	_TETNG Chromosome 1 SCAF15039, whole genome shotgun seq...	518 e-145
☐	tr	Q116X2	_TRIEI Phosphoglucomutase/phosphomannomutase alpha/beta...	518 e-145
☐	tr	Q93QE5	_RHILO Phosphoglucomutase (EC 5.4.2.2) [pgm] [Rhizobium...	518 e-145
☐	sp	Q9SCY0	PGMP_ARATH Phosphoglucomutase, chloroplast precursor (...	517 e-145
☐	tr	Q5CM20	_CRYHO Hypothetical protein [Chro.20343] [Cryptosporidi...	517 e-145
☐	tr	Q9EUT4	_RHITR Phosphoglucomutase (EC 5.4.2.2) [pgm] [Rhizobium...	516 e-144
☐	tr	Q16U43	_AEDAE Phosphoglucomutase [AaeL_AAEL010037] [Aedes aegy...	516 e-144
☐	tr	Q5CTF3	_CRYPV Phosphoglucomutase, tandemly duplicated gene (EC...	516 e-144
☐	sp	Q9SMM0	PGMP_BRANA Phosphoglucomutase, chloroplast precursor (...	515 e-144
☐	tr	Q21742	_CAEEL Hypothetical protein [R05F9.6] [Caenorhabditis e...	514 e-144
☐	sp	Q9SM60	PGMC_PEA Phosphoglucomutase, cytoplasmic (EC 5.4.2.2) ...	514 e-144
☐	tr	Q8G392	_BRUSU Phosphoglucomutase (EC 5.4.2.2) [pgm] [Brucella ...	513 e-143
☐	tr	Q57FV8	_BRUAB Pgm, phosphoglucomutase [pgm] [Brucella abortus]	513 e-143
☐	tr	Q2YPS4	_BRUA2 Phosphoglucomutase/phosphomannomutase:Phosphoglu...	513 e-143
☐	tr	Q8YEJ2	_BRUME PHOSPHOGLUCOMUTASE (EC 5.4.2.2) [BMEI1886] [Bruc...	513 e-143
☐	tr	Q93Y04	_ARATH Phosphoglucomutase [At1g23190/T26J12.5] [Arabido...	513 e-143
☐	tr	Q8VX48	_WHEAT Phosphoglucomutase (EC 5.4.2.2) (Fragment) [PGM]...	513 e-143
☐	tr	Q58I84	_AEDAE Phosphoglucomutase 1 [PGM1] [Aedes aegypti (Yell...	512 e-143
☐	tr	Q00UU5	_OSTTA Phosphoglucomutase (ISS) [Ot15g02630] [Ostreococ...	512 e-143
☐	sp	Q9SNX2	PGMC_BROIN Phosphoglucomutase, cytoplasmic (EC 5.4.2.2...	511 e-143
☐	sp	Q9SM59	PGMP_PEA Phosphoglucomutase, chloroplast precursor (EC...	510 e-143
☐	tr	Q1GZZ5	_METFK Phosphoglucomutase/phosphomannomutase alpha/beta...	510 e-143
☐	tr	Q8U8L6	_AGRT5 Phosphoglucomutase [pgm/exoC] [Agrobacterium tum...	509 e-142
☐	tr	Q7CU06	_AGRT5 AGR_L_1564p [AGR_L_1564] [Agrobacterium tumefaci...	509 e-142
☐	sp	P93262	PGMC_MESCR Phosphoglucomutase, cytoplasmic (EC 5.4.2.2...	509 e-142
☐	tr	Q9KIJ6	_BRUAB Phosphoglucomutase [pgm] [Brucella abortus]	508 e-142
☐	tr	Q1RZG1	_MEDTR Phosphoglucomutase/phosphomannomutase alpha/beta...	508 e-142
☐	tr	A4KQ73	_FRATU Phosphoglucomutase [FTHG_00461] [Francisella tul...	508 e-142
☐	tr	Q2A4U6	_FRATH Phosphoglucomutase [FTL_0484] [Francisella tular...	508 e-142
☐	tr	Q0BN66	_FRATO Phosphoglucomutase (EC 5.4.2.2) [pgm] [Francisel...	508 e-142

☐	tr	Q33AE4	_ORYSJ	Phosphoglucomutase, chloroplast, putative, expre...	508 e-142
☐	tr	Q53QR8	_ORYSJ	Phosphoglucomutase/phosphomannomutase, C-termina...	508 e-142
☐	tr	Q622A9	_CAEBR	Hypothetical protein CBG02267 [CBG02267] [Caenor...	507 e-142

Graphical overview of the alignments

Click here to resubmit your query after masking regions matching PROSITE profiles or Pfam HMMs
(? Help) (use ScanProsite for more details about PROSITE matches)



Alignments

sp P37012 PGM2_YEAST **Phosphoglucomutase-2 (EC 5.4.2.2) (Glucose phosphomutase 2) (PGM 2) [PGM2] [Saccharomyces cerevisiae (Baker's yeast)]** 569 AA align

Score = 1162 bits (3006), Expect = 0.0
Identities = 569/569 (100%), Positives = 569/569 (100%)

```
Query: 1   MSFQIETVPTKPYEDQKPGTSGLRKKTKVFKDEPNYTENFIQSIMEAIPEGSKGATLVVG 60
           MSFQIETVPTKPYEDQKPGTSGLRKKTKVFKDEPNYTENFIQSIMEAIPEGSKGATLVVG
Sbjct: 1   MSFQIETVPTKPYEDQKPGTSGLRKKTKVFKDEPNYTENFIQSIMEAIPEGSKGATLVVG 60

Query: 61  GDGRYYNDVILHKIAAIGAANGIKKLVIGQHGLLSTPAASHIMRTYEEKCTGGIILTASH 120
           GDGRYYNDVILHKIAAIGAANGIKKLVIGQHGLLSTPAASHIMRTYEEKCTGGIILTASH
Sbjct: 61  GDGRYYNDVILHKIAAIGAANGIKKLVIGQHGLLSTPAASHIMRTYEEKCTGGIILTASH 120

Query: 121 NPGGPENDMGIKYNLSNGGPAPESVTNAIWEISKKLTSYKIIKDFPELDLGTIGKNKKYG 180
           NPGGPENDMGIKYNLSNGGPAPESVTNAIWEISKKLTSYKIIKDFPELDLGTIGKNKKYG
Sbjct: 121 NPGGPENDMGIKYNLSNGGPAPESVTNAIWEISKKLTSYKIIKDFPELDLGTIGKNKKYG 180

Query: 181 PLLVDIIDITKDYVNFLKEIFDFDLIKKFIDNQRSTKNWKLLFDSMNGVTGPYGKAIFVD 240
           PLLVDIIDITKDYVNFLKEIFDFDLIKKFIDNQRSTKNWKLLFDSMNGVTGPYGKAIFVD
Sbjct: 181 PLLVDIIDITKDYVNFLKEIFDFDLIKKFIDNQRSTKNWKLLFDSMNGVTGPYGKAIFVD 240

Query: 241 EFGLPADEVLQNWHPSPDFGGMHPDPNLTYASSLVKRVDREKIEFGAASDGDGDRNMIYG 300
           EFGLPADEVLQNWHPSPDFGGMHPDPNLTYASSLVKRVDREKIEFGAASDGDGDRNMIYG
Sbjct: 241 EFGLPADEVLQNWHPSPDFGGMHPDPNLTYASSLVKRVDREKIEFGAASDGDGDRNMIYG 300

Query: 301 YGPSFVSPGDSVAIIAEYAAEIPYFAKQGIYGLARSFPTSGAIDRVAKAHGLNCYEVPTG 360
           YGPSFVSPGDSVAIIAEYAAEIPYFAKQGIYGLARSFPTSGAIDRVAKAHGLNCYEVPTG
Sbjct: 301 YGPSFVSPGDSVAIIAEYAAEIPYFAKQGIYGLARSFPTSGAIDRVAKAHGLNCYEVPTG 360

Query: 361 WKFFCALFDAKKLSICGEESFGTGSNHVREKDGVWAIMAWLNILAIYNKHHPENEASIKT 420
           WKFFCALFDAKKLSICGEESFGTGSNHVREKDGVWAIMAWLNILAIYNKHHPENEASIKT
Sbjct: 361 WKFFCALFDAKKLSICGEESFGTGSNHVREKDGVWAIMAWLNILAIYNKHHPENEASIKT 420

Query: 421 IQNEFWAKYGRTFFTRYDFEKVETEKANKIVDQLRAYVTKSGVVNSAFPADESLKVTDCG 480
           IQNEFWAKYGRTFFTRYDFEKVETEKANKIVDQLRAYVTKSGVVNSAFPADESLKVTDCG
Sbjct: 421 IQNEFWAKYGRTFFTRYDFEKVETEKANKIVDQLRAYVTKSGVVNSAFPADESLKVTDCG 480

Query: 481 DFSYTDLDGSVSDHQGLYVKLSNGARFVLRLSGTGSSGATIRLYIEKYCDDKSQYQKTAE 540
           DFSYTDLDGSVSDHQGLYVKLSNGARFVLRLSGTGSSGATIRLYIEKYCDDKSQYQKTAE
Sbjct: 481 DFSYTDLDGSVSDHQGLYVKLSNGARFVLRLSGTGSSGATIRLYIEKYCDDKSQYQKTAE 540

Query: 541 EYLKPIINSVIKFLNFKQVLGTEEPTVRT 569
           EYLKPIINSVIKFLNFKQVLGTEEPTVRT
Sbjct: 541 EYLKPIINSVIKFLNFKQVLGTEEPTVRT 569
```

tr Q5XQP0 Q5XQP0_SACKU **PGM2 [Saccharomyces kudriavzevii IFO 1802]** 569 AA align

Score = 1130 bits (2923), Expect = 0.0
Identities = 547/569 (96%), Positives = 565/569 (99%)

```
Query: 1   MSFQIETVPTKPYEDQKPGTSGLRKKTKVFKDEPNYTENFIQSIMEAIPEGSKGATLVVG 60
           MSFQIETVPTKPYEDQKPGTSGLRKKTKVFKD+PNYTENFIQSIMEAIPEGSKGATLVVG
Sbjct: 1   MSFQIETVPTKPYEDQKPGTSGLRKKTKVFKDQPNYTENFIQSIMEAIPEGSKGATLVVG 60

Query: 61  GDGRYYNDVILHKIAAIGAANGIKKLVIGQHGLLSTPAASHIMRTYEEKCTGGIILTASH 120
           GDGRYYNDVIL+KIAAIG+ANGIKKLVIGQ+GLLSTPAASHIMRTYEE+CTGGIILTASH
Sbjct: 61  GDGRYYNDVILNKIAAIGSANGIKKLVIGQYGLLSTPAASHIMRTYEEECTGGIILTASH 120

Query: 121 NPGGPENDMGIKYNLSNGGPAPESVTNAIWEISKKLTSYKIIKDFPELDLGTIGKNKKYG 180
           NPGGPENDMGIKYNLSNGGPAPESVTNAIW+ISKKLT+YKI+KDFPELDL TIGKNKKYG
Sbjct: 121 NPGGPENDMGIKYNLSNGGPAPESVTNAIWDISKKLTNYKIVKDFPELDLKTIGKNKKYG 180

Query: 181 PLLVDIIDITKDYVNFLKEIFDFDLIKKFIDNQRSTKNWKLLFDSMNGVTGPYGKAIFVD 240
           PLL+D+IDITK YV+FLK+IFDFDLIKKFIDNQRSTKNWKLLFDSMNGVTGPYGKAIFVD
Sbjct: 181 PLLIDVIDITKAYVDFLKKIFDFDLIKKFIDNQRSTKNWKLLFDSMNGVTGPYGKAIFVD 240

Query: 241 EFGLPADEVLQNWHPSPDFGGMHPDPNLTYASSLVKRVDREKIEFGAASDGDGDRNMIYG 300
           EFGLPA+EVLQNWHPSPDFGGMHPDPNLTYASSLVKRVDREKIEFGAASDGDGDRNMIYG
```

```
Sbjct: 241 EFGLPAEEVLQNWHPSPDFGGMHPDPNLTYASSLVKRVDREKIEFGAASDGDGDRNMIYG 300

Query: 301 YGPSFVSPGDSVAIIAEYAAEIPYFAKQGIYGLARSFPTSGAIDRVAKAHGLNCYEVPTG 360
           YGPSFVSPGDSVAIIAEYAAEIPYFAKQGIYGLARSFPTS AIDRVAKAHGLNCYEVPTG
Sbjct: 301 YGPSFVSPGDSVAIIAEYAAEIPYFAKQGIYGLARSFPTSAAIDRVAKAHGLNCYEVPTG 360

Query: 361 WKFFCALFDAKKLSICGEESFGTGSNHVREKDGVWAIMAWLNILAIYNKHHPENEASIKT 420
           WKFFCALFDAKKLSICGEESFGTGSNHVREKDGVWA+MAWLNILAIYNKHHPENEASIKT
Sbjct: 361 WKFFCALFDAKKLSICGEESFGTGSNHVREKDGVWAVMAWLNILAIYNKHHPENEASIKT 420

Query: 421 IQNEFWAKYGRTFFTRYDFEKVETEKANKIVDQLRAYVTKSGVVNSAFPADESLKVTDCG 480
           IQNEFWAKYGRTFFTRYDFEKVE+EKANKIVDQLRAYVTKSGV+NSAFPADESLKVTDCG
Sbjct: 421 IQNEFWAKYGRTFFTRYDFEKVESEKANKIVDQLRAYVTKSGVINSAFPADESLKVTDCG 480

Query: 481 DFSYTDLDGSVSDHQGLYVKLSNGARFVLRLSGTGSSGATIRLYIEKYCDDKSQYQKTAE 540
           DFSYTDLDGSVSDHQGLYVKLSNGARFVLRLSGTGSSGATIRLY+EKYCDDKSQYQKTAE
Sbjct: 481 DFSYTDLDGSVSDHQGLYVKLSNGARFVLRLSGTGSSGATIRLYVEKYCDDKSQYQKTAE 540

Query: 541 EYLKPIINSVIKFLNFKQVLGTEEPTVRT 569
           EYLKPIINSVIKFL FKQVLGT+EPTVRT
Sbjct: 541 EYLKPIINSVIKFLKFKQVLGTDEPTVRT 569
```

tr Q6FN21_CANGA — **Similar to sp|P37012 Saccharomyces cerevisiae YMR105c Phosphoglucomutase 2 [CAGL0K03421g] [Candida glabrata (Yeast) (Torulopsis glabrata)]** — 568 AA, align

Score = 977 bits (2526), Expect = 0.0
Identities = 466/566 (82%), Positives = 510/566 (90%)

```
Query: 4   QIETVPTKPYEDQKPGTSGLRKKTKVFKDEPNYTENFIQSIMEAIPEGSKGATLVVGGDG 63
           QIE+VPTKPY+DQKPGTSGLRKKTKVF+D+PNY ENFIQS+MEAIPEG+KGA LVVGGDG
Sbjct: 3   QIESVPTKPYQDQKPGTSGLRKKTKVFEDQPNYVENFIQSVMEAIPEGAKGAVLVVGGDG 62

Query: 64  RYYNDVILHKIAAIGAANGIKKLVIGQHGLLSTPAASHIMRTYEEKCTGGIILTASHNPG 123
           RYYNDVIL KIAAIGAANG+KKLVIGQ+GLLSTPAASHIMRTY+EKCTGGIILTASHNPG
Sbjct: 63  RYYNDVILQKIAAIGAANGVKKLVIGQNGLLSTPAASHIMRTYKEKCTGGIILTASHNPG 122

Query: 124 GPENDMGIKYNLSNGGPAPESVTNAIWEISKKLTSYKIIKDFPELDLGTIGKNKKYGPLL 183
           GPENDMGIKYNLSNGGPAPE VTN IWEISKKLT YKI+KDFPELDL  + +NKKYGPLL
Sbjct: 123 GPENDMGIKYNLSNGGPAPEPVTNKIWEISKKLTHYKIVKDFPELDLTKLVENKKYGPLL 182

Query: 184 VDIIDITKDYVNFLKEIFDFDLIKKFIDNQRSTKNWKLLFDSMNGVTGPYGKAIFVDEFG 243
           VD+ID T  Y+  LKEIFDF+LI KFI  QR  K WKLL DSMNGVTGPY KAIFVDEFG
Sbjct: 183 VDVIDTTDAYIQLLKEIFDFELIHKFIAKQRKEKGWKLLVDSMNGVTGPYAKAIFVDEFG 242

Query: 244 LPADEVLQNWHPSPDFGGMHPDPNLTYASSLVKRVDREKIEFGAASDGDGDRNMIYGYGP 303
           L + EVLQNWHP PDFGG+HPDPNLTYA +LV+RV++EKIEFGAASDGDGDRNMIYGYGP
Sbjct: 243 LDSKEVLQNWHPQPDFGGLHPDPNLTYAHTLVERVNKEKIEFGAASDGDGDRNMIYGYGP 302

Query: 304 SFVSPGDSVAIIAEYAAEIPYFAKQGIYGLARSFPTSGAIDRVAKAHGLNCYEVPTGWKF 363
           +FVSPGDSVAIIAEYA EIPYF KQGIYGLARSFPT+ AIDRVAK HGLNCYEVPTGWKF
Sbjct: 303 AFVSPGDSVAIIAEYANEIPYFKKQGIYGLARSFPTASAIDRVAKKHGLNCYEVPTGWKF 362

Query: 364 FCALFDAKKLSICGEESFGTGSNHVREKDGVWAIMAWLNILAIYNKHHPENEASIKTIQN 423
           FCALFDAKKLSICGEESFGTGSNHVREKDG+WAIMAWLNILAI+N+ HP+ EASIKTIQN
Sbjct: 363 FCALFDAKKLSICGEESFGTGSNHVREKDGIWAIMAWLNILAIFNQRHPDKEASIKTIQN 422

Query: 424 EFWAKYGRTFFTRYDFEKVETEKANKIVDQLRAYVTKSGVVNSAFPADESLKVTDCGDFS 483
           EFW  YGRTFFTRYD+EKVET+KANK++  LR YV  SG   S FP D +L V D GDFS
Sbjct: 423 EFWDTYGRTFFTRYDYEKVETDKANKVIENLRQYVADSGTKGSKFPTDSALTVVDAGDFS 482

Query: 484 YTDLDGSVSDHQGLYVKLSNGARFVLRLSGTGSSGATIRLYIEKYCDDKSQYQKTAEEYL 543
           YTDLDG++S HQGLYV LSNGARFV+RLSGTGSSGATIRLYIE+Y DDKS+Y   A+EYL
Sbjct: 483 YTDLDGTISSHQGLYVILSNGARFVVRLSGTGSSGATIRLYIERYTDDKSKYSLDAQEYL 542

Query: 544 KPIINSVIKFLNFKQVLGTEEPTVRT 569
           KPII S+++FL+ K +LGTEEPTVRT
Sbjct: 543 KPIIKSIVQFLDLKTILGTEEPTVRT 568
```

tr Q6FMJ8_CANGA — **Similar to sp|P37012 Saccharomyces cerevisiae YMR105c PGM2 phosphoglucomutase [CAGL0K07480g] [Candida glabrata (Yeast) (Torulopsis glabrata)]** — 567 AA, align

Score = 977 bits (2525), Expect = 0.0
Identities = 461/566 (81%), Positives = 517/566 (91%)

```
Query: 4   QIETVPTKPYEDQKPGTSGLRKKTKVFKDEPNYTENFIQSIMEAIPEGSKGATLVVGGDG 63
           Q+ETVPTKPY+DQKPGTSGLRKKTKVF +EPNYTENFIQ+IM+AIPEG+K A LVVGGDG
Sbjct: 2   QVETVPTKPYQDQKPGTSGLRKKTKVFMEEPNYTENFIQAIMDAIPEGAKDAVLVVGGDG 61
```

```
Query: 64  RYYNDVILHKIAAIGAANGIKKLVIGQHGLLSTPAASHIMRTYEEKCTGGIILTASHNPG 123
           R+YNDVI+ KIAAIGAANG++KL+IGQ+GLLSTPAASH++R+Y EKCTGGIILTASHNPG
Sbjct: 62  RFYNDVIMQKIAAIGAANGVRKLIIGQNGLLSTPAASHVIRSYAEKCTGGIILTASHNPG 121

Query: 124 GPENDMGIKYNLSNGGPAPESVTNAIWEISKKLTSYKIIKDFPELDLGTIGKNKKYGPLL 183
           GPEND+GIKYNL+NGGPAPE VTN +WE+SK+LT YKIIKDFP++D   IGK+++YGPLL
Sbjct: 122 GPENDLGIKYNLANGGPAPEPVTNKMWEVSKQLTHYKIIKDFPQVDFSKIGKDQQYGPLL 181

Query: 184 VDIIDITKDYVNFLKEIFDFDLIKKFIDNQRSTKNWKLLFDSMNGVTGPYGKAIFVDEFG 243
           VDIID T+DYV F+KEIFDF LIK+FI  QR  KNWKLLFDS+NG+TGPYGKAIFVDEF
Sbjct: 182 VDIIDTTEDYVKFMKEIFDFKLIKEFIHKQREAKNWKLLFDSLNGITGPYGKAIFVDEFD 241

Query: 244 LPADEVLQNWHPSPDFGGMHPDPNLTYASSLVKRVDREKIEFGAASDGDGDRNMIYGYGP 303
           LPADEVLQNWHP PDFGG+HPDPNLTYA +LV+RVDREKIEFGAASDGDGDRNMIYG GP
Sbjct: 242 LPADEVLQNWHPQPDFGGLHPDPNLTYAHTLVERVDREKIEFGAASDGDGDRNMIYGAGP 301

Query: 304 SFVSPGDSVAIIAEYAAEIPYFAKQGIYGLARSFPTSGAIDRVAKAHGLNCYEVPTGWKF 363
           +FVSPGDSVAIIAEYA EIPYF KQGIYGLARSFPTSGAIDRVAKA GLNCYEVPTGWKF
Sbjct: 302 AFVSPGDSVAIIAEYAKEIPYFQKQGIYGLARSFPTSGAIDRVAKAQGLNCYEVPTGWKF 361

Query: 364 FCALFDAKKLSICGEESFGTGSNHVREKDGVWAIMAWLNILAIYNKHHPENEASIKTIQN 423
           FCALFDAKKLSICGEESFGTGSNH+REKDGVWAI AWLNILA+YNKH+PE EASIKTIQ
Sbjct: 362 FCALFDAKKLSICGEESFGTGSNHIREKDGVWAICAWLNILALYNKHNPEKEASIKTIQE 421

Query: 424 EFWAKYGRTFFTRYDFEKVETEKANKIVDQLRAYVTKSGVVNSAFPADESLKVTDCGDFS 483
           EFWAKYGRTFFTRYD+E + TEKANK+VD L  +V       N+ FP DESL V+DCGDFS
Sbjct: 422 EFWAKYGRTFFTRYDYEGITTEKANKVVDLLDKFVNDPKSKNAPFPGDESLTVSDCGDFS 481

Query: 484 YTDLDGSVSDHQGLYVKLSNGARFVLRLSGTGSSGATIRLYIEKYCDDKSQYQKTAEEYL 543
           YTDLDGSVSDHQGL+VKLSNGARFVLRLSGTGS+GATIRLYIE+Y DDKS Y ++A++YL
Sbjct: 482 YTDLDGSVSDHQGLFVKLSNGARFVLRLSGTGSAGATIRLYIEEYSDDKSTYTQSADQYL 541

Query: 544 KPIINSVIKFLNFKQVLGTEEPTVRT 569
           + +I SV  FLNFK+++GT+EPTVRT
Sbjct: 542 QKMIKSVTSFLNFKELIGTDEPTVRT 567
```

sp P33401 Phosphoglucomutase-1 (EC 5.4.2.2) (Glucose phosphomutase 1) (PGM 1) 570 AA
PGM1_YEAST [PGM1] [Saccharomyces cerevisiae (Baker's yeast)] align

Score = 943 bits (2438), Expect = 0.0
Identities = 450/570 (78%), Positives = 508/570 (89%), Gaps = 1/570 (0%)

```
Query: 1   MSFQIETVPTKPYEDQKPGTSGLRKKTKVFKDEPNYTENFIQSIMEAIPEGSKGATLVVG 60
           MS  I++VPT  Y+DQKPGTSGLRKKTKVF DEP+YTENFIQ+ M++IP GS+G TLVVG
Sbjct: 1   MSLLIDSVPTVAYKDQKPGTSGLRKKTKVFMDEPHYTENFIQATMQSIPNGSEGTTLVVG 60

Query: 61  GDGRYYNDVILHKIAAIGAANGIKKLVIGQHGLLSTPAASHIMRTYEEKCTGG-IILTAS 119
           GDGR+YNDVI++KIAA+GAANG++KLVIGQ GLLSTPAASHI+RTYEEKCTGG IILTAS
Sbjct: 61  GDGRFYNDVIMNKIAAVGAANGVRKLVIGQGGLLSTPAASHIIRTYEEKCTGGGIILTAS 120

Query: 120 HNPGGPENDMGIKYNLSNGGPAPESVTNAIWEISKKLTSYKIIKDFPELDLGTIGKNKKY 179
           HNPGGPEND+GIKYNL NGGPAPESVTNAIWE SKKLT YKIIK+FP+L+L  +GKN+KY
Sbjct: 121 HNPGGPENDLGIKYNLPNGGPAPESVTNAIWEASKKLTHYKIIKNFPKLNLNKLGKNQKY 180

Query: 180 GPLLVDIIDITKDYVNFLKEIFDFDLIKKFIDNQRSTKNWKLLFDSMNGVTGPYGKAIFV 239
           GPLLVDIID  K YV FLKEIFDFDLIK F+  QR  K WKLLFDS+NG+TGPYGKAIFV
Sbjct: 181 GPLLVDIIDPAKAYVQFLKEIFDFDLIKSFLAKQRKDKGWKLLFDSLNGITGPYGKAIFV 240

Query: 240 DEFGLPADEVLQNWHPSPDFGGMHPDPNLTYASSLVKRVDREKIEFGAASDGDGDRNMIY 299
           DEFGLPA+EVLQNWHP PDFGG+HPDPNLTYA +LV RVDREKI FGAASDGDGDRNMIY
Sbjct: 241 DEFGLPAEEVLQNWHPLPDFGGLHPDPNLTYARTLVDRVDREKIAFGAASDGDGDRNMIY 300

Query: 300 GYGPSFVSPGDSVAIIAEYAAEIPYFAKQGIYGLARSFPTSGAIDRVAKAHGLNCYEVPT 359
           GYGP+FVSPGDSVAIIAEYA EIPYFAKQGIYGLARSFPTS AIDRVA   GL CYEVPT
Sbjct: 301 GYGPAFVSPGDSVAIIAEYAPEIPYFAKQGIYGLARSFPTSSAIDRVAAKKGLRCYEVPT 360

Query: 360 GWKFFCALFDAKKLSICGEESFGTGSNHVREKDGVWAIMAWLNILAIYNKHHPENEASIK 419
           GWKFFCALFDAKKLSICGEESFGTGSNH+REKDG+WAI+AWLNILAIY++ +PE EASIK
Sbjct: 361 GWKFFCALFDAKKLSICGEESFGTGSNHIREKDGLWAIIAWLNILAIYHRRNPEKEASIK 420

Query: 420 TIQNEFWAKYGRTFFTRYDFEKVETEKANKIVDQLRAYVTKSGVVNSAFPADESLKVTDC 479
           TIQ+EFW +YGRTFFTRYD+E +E E+A K+V  L  +V++  V  S FPADESL V DC
Sbjct: 421 TIQDEFWNEYGRTFFTRYDYEHIECEQAEKVVALLSEFVSRPNVCGSHFPADESLTVIDC 480

Query: 480 GDFSYTDLDGSVSDHQGLYVKLSNGARFVLRLSGTGSSGATIRLYIEKYCDDKSQYQKTA 539
           GDFSY DLDGS+S++QGL+VK SNG +FVLRLSGTGSSGATIRLY+EKY D K  Y +TA
Sbjct: 481 GDFSYRDLDGSISENQGLFVKFSNGTKFVLRLSGTGSSGATIRLYVEKYTDKKENYGQTA 540

Query: 540 EEYLKPIINSVIKFLNFKQVLGTEEPTVRT 569
           + +LKP+INS++KFL FK++LGT+EPTVRT
Sbjct: 541 DVFLKPVINSIVKFLRFKEILGTDEPTVRT 570
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```
tr  Q5XQP1        PGM1 (Fragment) [Saccharomyces kudriavzevii IFO 1802]  548 AA
    Q5XQP1_SACKU                                                        align

 Score =  923 bits (2385), Expect = 0.0
 Identities = 439/548 (80%), Positives = 492/548 (89%), Gaps = 1/548 (0%)

Query: 23  LRKKTKVFKDEPNYTENFIQSIMEAIPEGSKGATLVVGGDGRYYNDVILHKIAAIGAANG 82
           LRKKTKVF +EP+YTENFIQ++ME+IP G  GATLVVGGDGR+YNDVI++KIAA+GAANG
Sbjct: 1   LRKKTKVFMNEPHYTENFIQAMMESIPNGPDGATLVVGGDGRFYNDVIMNKIAAVGAANG 60

Query: 83  IKKLVIGQHGLLSTPAASHIMRTYEEKCTGG-IILTASHNPGGPENDMGIKYNLSNGGPA 141
           I+KL+IGQ GLLSTPAASHI+RTYE++C GG IILTASHNPGGPEND+GIKYNL NGGPA
Sbjct: 61  IRKLIIGQGGLLSTPAASHIIRTYEDRCNGGGIILTASHNPGGPENDLGIKYNLRNGGPA 120

Query: 142 PESVTNAIWEISKKLTSYKIIKDFPELDLGTIGKNKKYGPLLVDIIDITKDYVNFLKEIF 201
           PESVTNAIWE SKKLT YKI+ +FPELD+  +GKN+ YGPLLVDIID  + YV FLKEIF
Sbjct: 121 PESVTNAIWEASKKLTHYKIVTNFPELDMNKLGKNQNYGPLLVDIIDPARAYVQFLKEIF 180

Query: 202 DFDLIKKFIDNQRSTKNWKLLFDSMNGVTGPYGKAIFVDEFGLPADEVLQNWHPSPDFGG 261
           DFDLIK F+  QR TK WKLLFDS+NG+TGPYGKAIFVDEFGLPA+EVLQNWHP PDFGG
Sbjct: 181 DFDLIKSFLTEQRRTKGWKLLFDSLNGITGPYGKAIFVDEFGLPAEEVLQNWHPLPDFGG 240

Query: 262 MHPDPNLTYASSLVKRVDREKIEFGAASDGDGDRNMIYGYGPSFVSPGDSVAIIAEYAAE 321
           +HPDPNLTYA +LV RVDREKI FGAASDGDGDRNMIYGYGP+FVSPGDSVAIIAEYA+E
Sbjct: 241 LHPDPNLTYARTLVSRVDREKIAFGAASDGDGDRNMIYGYGPAFVSPGDSVAIIAEYASE 300

Query: 322 IPYFAKQGIYGLARSFPTSGAIDRVAKAHGLNCYEVPTGWKFFCALFDAKKLSICGEESF 381
           IPYFAKQGIYGLARSFPTS AIDRVA   GLNCYEVPTGWKFFCALFDA KLSICGEESF
Sbjct: 301 IPYFAKQGIYGLARSFPTSSAIDRVAAKKGLNCYEVPTGWKFFCALFDANKLSICGEESF 360

Query: 382 GTGSNHVREKDGVWAIMAWLNILAIYNKHHPENEASIKTIQNEFWAKYGRTFFTRYDFEK 441
           GTGSNH+REKDG+WAI+AWLNILAIYNKH+PE EASIKTIQ+EFW +YGRTFFTRYD+E
Sbjct: 361 GTGSNHIREKDGIWAIIAWLNILAIYNKHNPEKEASIKTIQDEFWNEYGRTFFTRYDYEH 420

Query: 442 VETEKANKIVDQLRAYVTKSGVVNSAFPADESLKVTDCGDFSYTDLDGSVSDHQGLYVKL 501
           +E E+A K+V  L  +VTK  VV   FP DESL V DCGDFSYTDLDGS+S+ QGL+VKL
Sbjct: 421 LECEQAEKVVALLNNFVTKPDVVGCQFPGDESLTVADCGDFSYTDLDGSISEKQGLFVKL 480

Query: 502 SNGARFVLRLSGTGSSGATIRLYIEKYCDDKSQYQKTAEEYLKPIINSVIKFLNFKQVLG 561
           SNGA+FVLRLSGTGSSGATIRLY+EKY D+K  Y +TAE +LKPIINS++KFL F+++LG
Sbjct: 481 SNGAKFVLRLSGTGSSGATIRLYVEKYTDNKGNYDETAEIFLKPIINSIVKFLKFEEILG 540

Query: 562 TEEPTVRT 569
           TEEPTVRT
Sbjct: 541 TEEPTVRT 548
```

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tr  Q6CVE3        Similar to sp|P37012 Saccharomyces cerevisiae YMR105c PGM2  568 AA
    Q6CVE3_KLULA  phosphoglucomutase [KLLA0B12694g] [Kluyveromyces lactis     align
                  (Yeast) (Candida sphaerica)]

 Score =  871 bits (2250), Expect = 0.0
 Identities = 419/570 (73%), Positives = 488/570 (85%), Gaps = 3/570 (0%)

Query: 1   MSFQIETVPTKPYEDQKPGTSGLRKKTKVFKDEPNYTENFIQSIMEAIPEGSKGATLVVG 60
           MS +  +V T PY DQKPGTSGLRKKTKVF++ PNYTENFIQ+IMEAIPEGS+GATLV+G
Sbjct: 1   MSLKTVSVATNPYPDQKPGTSGLRKKTKVFEETPNYTENFIQAIMEAIPEGSQGATLVIG 60

Query: 61  GDGRYYNDVILHKIAAIGAANGIKKLVIGQHGLLSTPAASHIMRTYEEKCTGGIILTASH 120
           GDGRYYNDV++ KIAAIG+ANG++K+VIG +G+LSTPAASHI+R Y EKCTGGIILTASH
Sbjct: 61  GDGRYYNDVVIQKIAAIGSANGVRKIVIGHNGILSTPAASHIIRAYHEKCTGGIILTASH 120

Query: 121 NPGGPENDMGIKYNLSNGGPAPESVTNAIWEISKKLTSYKIIKDFPELDLGTIGKNKKYG 180
           NPGGP ND GIKYNL+NGGPAPESVTN+IW  S++LT YKI++ FP +DL  IG+++KYG
Sbjct: 121 NPGGPTNDFGIKYNLANGGPAPESVTNSIWHKSRELTHYKIVESFPAIDLTKIGQDQKYG 180

Query: 181 PLLVDIIDITKDYVNFLKEIFDFDLIKKFIDNQRSTKNWKLLFDSMNGVTGPYGKAIFVD 240
            LLVDI+D T  YV  +KEIFDF LIK FID Q +   +K+LFD+MNGVTGPYG+A+FV
Sbjct: 181 DLLVDIVDSTAAYVELMKEIFDFPLIKSFIDTQ-AKNGFKILFDAMNGVTGPYGEALFVK 239

Query: 241 EFGLPADEVLQNWHPSPDFGGMHPDPNLTYASSLVKRVDREKIEFGAASDGDGDRNMIYG 300
           E GLP +  LQN+HP PDFGG+HPDPNLTYA +LV+RVD+  I+FGAASDGDGDRNMIYG
Sbjct: 240 ELGLP-ESSLQNYHPKPDFGGLHPDPNLTYAHTLVERVDKYGIQFGAASDGDGDRNMIYG 298

Query: 301 YGPSFVSPGDSVAIIAEYAAEIPYFAKQGIYGLARSFPTSGAIDRVAKAHGLNCYEVPTG 360
            GP+FVSPGDSVAIIAEYA+ IPYF KQGIYGLARSFPTS AIDRVAK  GLNCYEVPTG
Sbjct: 299 AGPAFVSPGDSVAIIAEYASAIPYFKKQGIYGLARSFPTSSAIDRVAKEQGLNCYEVPTG 358

Query: 361 WKFFCALFDAKKLSICGEESFGTGSNHVREKDGVWAIMAWLNILAIYNKHHPENEASIKT 420
           WKFFCALFDAKKLSICGEESFGTGSNHVREKDGVWAIMAWLNILAIYN+  P  EASIK+
Sbjct: 359 WKFFCALFDAKKLSICGEESFGTGSNHVREKDGVWAIMAWLNILAIYNQRFPNKEASIKS 418

Query: 421 IQNEFWAKYGRTFFTRYDFEKVETEKANKIVDQLRAYVT-KSGVVNSAFPADESLKVTDC 479
```